



SEQUENCE LISTING

<110> Mosselman, Sietse
Dijkema, Rein

<120> Novel Estrogen Receptor

<130> O/96193 US

<150> US 08/826,361

<151> 1997-03-26

<150> EP 96203284.3

<151> 1996-11-22

<150> EP 96200820.7

<151> 1996-03-26

<160> 32

<170> PatentIn version 3.0

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 20 25 30

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Gly Met
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 20 25 30

Lys Leu Ala Asp Lys Glu Leu Val His Met Ile Ser Trp Ala Lys Lys
 35 40 45

Ile Pro Gly Phe Val Glu Leu Ser Leu Phe Asp Gln Val Arg Leu Leu
 50 55 60

Glu Ser Cys Trp Met Glu Val Leu Met Met Gly Leu Met Trp Arg Ser
 65 70 75 80

Ile Asp His Pro Gly Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp
 85 90 95

Arg Asp Glu Gly Lys Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met
 100 105 110

Leu Leu Ala Thr Thr Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys
 115 120 125

Glu Tyr Leu Cys Val Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr
 130 135 140

Pro Leu Val Thr Ala Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala
 145 150 155 160

His Leu Leu Asn Ala Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys
 165 170 175

Ser Gly Ile Ser Ser Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu
 180 185 190

Met Leu Leu Ser His Val Arg His Ala Ser Asn Lys Gly Met Glu His
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35 40 45
Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser Leu Glu His Thr Leu
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Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val Ser Gly Asn Arg Cys
65 70 75 80
Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg Asp Ala His Phe Cys
85 90 95
Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser
100 105 110
Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn
115 120 125
Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg
130 135 140
Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly
145 150 155 160
Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg Leu Val
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Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly Lys Ala
180 185 190
Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg Glu Leu Leu Leu Asp
195 200 205
Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu Leu Glu Ala Glu Pro
210 215 220
Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro Phe Thr Glu Ala Ser
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Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys Glu Leu Val His Met
245 250 255
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260 265 270
Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met Glu Val Leu Met Met
275 280 285
Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly Lys Leu Ile Phe Ala

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Leu	Lys	Leu	Gln	His	Lys	Glu	Tyr	Leu	Cys	Val	Lys	Ala	Met	Ile	Leu
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Arg	Leu	Ala	Asn	Leu	Leu	Met	Leu	Leu	Ser	His	Val	Arg	His	Ala	Ser
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Pro	Gln	Lys	Ser	Pro	Trp	Cys	Glu	Ala	Arg	Ser	Leu	Glu	His	Thr	Leu
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Ala	Ser	Pro	Val	Thr	Gly	Pro	Gly	Ser	Lys	Arg	Asp	Ala	His	Phe	Cys
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Ala	Val	Cys	Ser	Asp	Tyr	Ala	Ser	Gly	Tyr	His	Tyr	Gly	Val	Trp	Ser
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165                      170                      175

Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly Lys Ala
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Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg Glu Leu Leu Leu Asp
195                      200                      205

Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu Leu Glu Ala Glu Pro
210                      215                      220

Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro Phe Thr Glu Ala Ser
225                      230                      235                      240

Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys Glu Leu Val His Met
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Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Phe
260                      265                      270

Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met Glu Val Leu Met Met
275                      280                      285

Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly Lys Leu Ile Phe Ala
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Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys Cys Val Glu Gly Ile
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Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr Ser Arg Phe Arg Glu
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Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val Lys Ala Met Ile Leu
340                      345                      350

Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala Thr Gln Asp Ala Asp
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Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala Val Thr Asp Ala Leu
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Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser Gln Gln Gln Ser Met
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          20          25          30

Leu Ser Pro Leu Val Val  His Arg Gln Leu Ser His Leu Tyr Ala Glu
          35          40          45

Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser Leu Glu His Thr Leu
          50          55          60

Pro Val Asn Arg Glu  Thr Leu Lys Arg Lys Val Ser Gly Asn Arg Cys
          65          70          75          80

Ala Ser Pro Val  Thr Gly Pro Gly Ser  Lys Arg Asp Ala His Phe Cys
          85          90          95

Ala Val Cys Ser  Asp Tyr Ala Ser  Gly Tyr His Tyr Gly Val Trp Ser
          100         105         110

Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn
          115         120         125

Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg
          130         135         140

Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly
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Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg Leu Val
          165         170         175

Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly Lys Ala

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Pro	His	Val	Leu	Ile	Ser	Arg	Pro	Ser	Ala	Pro	Phe	Thr	Glu	Ala	Ser				
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Gly	Leu	Met	Trp	Arg	Ser	Ile	Asp	His	Pro	Gly	Lys	Leu	Ile	Phe	Ala				
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Pro	Asp	Leu	Val	Leu	Asp	Arg	Asp	Glu	Gly	Lys	Cys	Val	Glu	Gly	Ile				
305					310					315					320				
Leu	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	Thr	Ser	Arg	Phe	Arg	Glu				
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Leu	Lys	Leu	Gln	His	Lys	Glu	Tyr	Leu	Cys	Val	Lys	Ala	Met	Ile	Leu				
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Ser	Ser	Arg	Lys	Leu	Ala	His	Leu	Leu	Asn	Ala	Val	Thr	Asp	Ala	Leu				
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Val	Trp	Val	Ile	Ala	Lys	Ser	Gly	Ile	Ser	Ser	Gln	Gln	Gln	Ser	Met				
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Ser Ala

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agcgacccag gatgctgaca gcagccggaa gctggctcac ttgctgaacg ccgtgaccga	1380
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tctgctcaac atgaagtga aaaatgtggc cccagtgtat gacctgtgc tggagatgct	1560
gaatgccac gtgcttcgcg ggtgcaagtc ctccatcacg gggtcgagt gcagcccggc	1620
agaggacagt aaaagcaaag agggctccca gaaccacag tctcagtgc gcctggccct	1680
gaggtgaact ggccacaga ggtcacaagc tgaagcgtga actccagtgt gtcaggagcc	1740
tgggcttcat ctttctgctg tgtggtccct catttggtga tggcaggctt ggtcatgtac	1800

catccttccc tccaccttcc caactctcag gattcggtgt gaggaagcca tagtttccct 1860

tgtttagcaga gggacatttg aatcgagcgt ttccacac 1898

<210> 25

<211> 530

<212> PRT

<213> Homo sapiens

<400> 25

Met Asp Ile Lys Asn Ser Pro Ser Ser Leu Asn Ser Pro Ser Ser Tyr
1 5 10 15

Asn Cys Ser Gln Ser Ile Leu Pro Leu Glu His Gly Ser Ile Tyr Ile
20 25 30

Pro Ser Ser Tyr Val Asp Ser His His Glu Tyr Pro Ala Met Thr Phe
35 40 45

Tyr Ser Pro Ala Val Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn
50 55 60

Leu Glu Gly Gly Pro Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp
65 70 75 80

Pro Thr Pro Gly His Leu Ser Pro Leu Val Val His Arg Gln Leu Ser
85 90 95

His Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser
100 105 110

Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val
115 120 125

Ser Gly Asn Arg Cys Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg
130 135 140

Asp Ala His Phe Cys Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His
145 150 155 160

Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser
165 170 175

Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr
180 185 190

Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys
195 200 205

Cys Tyr Glu Val Gly Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys
210 215 220

Gly Tyr Arg Leu Val Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His
225 230 235 240

Cys Ala Gly Lys Ala Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg
245 250 255

Glu Leu Leu Leu Asp Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu
260 265 270

Leu Glu Ala Glu Pro Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro
275 280 285

Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys
 290 295 300
 Glu Leu Val His Met Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val
 305 310 315 320
 Glu Leu Ser Leu Phe Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met
 325 330 335
 Glu Val Leu Met Met Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly
 340 345 350
 Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys
 355 360 365
 Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr
 370 375 380
 Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val
 385 390 395 400
 Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala
 405 410 415
 Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala
 420 425 430
 Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser
 435 440 445
 Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His
 450 455 460
 Val Arg His Ala Ser Asn Lys Gly Met Glu His Leu Leu Asn Met Lys
 465 470 475 480
 Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu Leu Glu Met Leu Asn
 485 490 495
 Ala His Val Leu Arg Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys
 500 505 510
 Ser Pro Ala Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln
 515 520 525

Ser Gln
530

<210> 26
 <211> 30
 <212> DNA
 <213> Homo sapiens

<400> 26
 gtgcgatcc tctcaagaca tggatataaa

30

<210> 27
 <211> 25
 <212> DNA
 <213> Homo sapiens

<400> 27
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25

<210> 28
 <211> 22
 <212> DNA
 <213> Homo sapiens

<400> 28
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22

<210> 29
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 <212> DNA
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<220>
 <223> Description of Artificial Sequence: oligonucleotide

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20

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<220>
 <223> Description of Artificial Sequence: oligonucleotide

<400> 30
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18

<210> 31
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 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: oligonucleotide

<400> 31
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21

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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: oligonucleotide

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21